1/29

#2

OIPE

RAW SEQUENCE LISTING                    DATE: 02/15/2002
PATENT APPLICATION:  US/10/017,910      TIME: 15:47:43

Input Set : N:\Crf3\RULE60\10017910.txt
Output Set: N:\CRF3\02152002\J017910.raw

```
                    SEQUENCE LISTING
 4 (1) GENERAL INFORMATION:
 6      (i) APPLICANT: Choi, Yongwon
 7                    Wong, Brian
 8                    Josien, Regis
 9                    Steinman, Ralph
11     (ii) TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
12                             INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
SAME, AND
13                             METHODS OF USE THEREOF
15    (iii) NUMBER OF SEQUENCES: 14
17     (iv) CORRESPONDENCE ADDRESS:
18          (A) ADDRESSEE: Klauber & Jackson
19          (B) STREET: 411 Hackensack Avenue, 4th Floor
20          (C) CITY: Hackensack
21          (D) STATE: New Jersey
22          (E) COUNTRY: USA
23          (F) ZIP: 07601
25      (v) COMPUTER READABLE FORM:
26          (A) MEDIUM TYPE: Floppy disk
27          (B) COMPUTER: IBM PC compatible
28          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
31     (vi) CURRENT APPLICATION DATA:        .
C--> 32          (A) APPLICATION NUMBER: US/10/017,910
C--> 33          (B) FILING DATE: 14-Dec-2001
39          (C) CLASSIFICATION:
36    (vii) PRIOR APPLICATION DATA:
37          (A) APPLICATION NUMBER: US 09/447,035
38          (B) FILING DATE: 1999-11-22
41   (viii) ATTORNEY/AGENT INFORMATION:
42          (A) NAME: Jackson Esq., David A.
43          (B) REGISTRATION NUMBER: 26,742
44          (C) REFERENCE/DOCKET NUMBER: 600-1-200
46     (ix) TELECOMMUNICATION INFORMATION:
47          (A) TELEPHONE: 201-487-5800
48          (B) TELEFAX: 201-343-1684
49          (C) TELEX: 133521
52 (2) INFORMATION FOR SEQ ID NO: 1:
54      (i) SEQUENCE CHARACTERISTICS:
55          (A) LENGTH: 1823 base pairs
56          (B) TYPE: nucleic acid
57          (C) STRANDEDNESS: double
58          (D) TOPOLOGY: linear
```

ENTERED

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60      (ii) MOLECULE TYPE: cDNA
62     (iii) HYPOTHETICAL: NO
64      (vi) ORIGINAL SOURCE:
65           (A) ORGANISM: Homo sapiens
67      (ix) FEATURE:
68           (A) NAME/KEY: CDS
69           (B) LOCATION: 1..738
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74 CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT        48
75 Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
76  1               5                  10                  15
78 AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG        96
79 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
80              20                  25                  30
82 GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA       144
83 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
84          35                  40                  45
86 CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA       192
87 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
88      50                  55                  60
90 TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA       240
91 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
92  65                  70                  75                  80
94 GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC       288
95 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
96  .              85                  90                  95
98 ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG       336
99 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
100             100                 105                 110
102 TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT      384
103 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
104             115                 120                 125
106 TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG      432
107 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
108     130                 135                 140
110 TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT      480
111 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
112 145                 150                 155                 160
114 ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA      528
115 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
116                 165                 170                 175
118 ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG      576
119 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
120             180                 185                 190
122 TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT      624
123 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
124         195                 200                 205
126 TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC      672
127 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
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Input Set : N:\Crf3\RULE60\10017910.txt
Output Set: N:\CRF3\02152002\J017910.raw

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128     210                 215                 220
130 TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA        720
131 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
132 225                 230                 235                 240
134 GTT CGA GAT ATA GAT TGA GCCCCAGTTT TTGGAGTGTT ATGTATTTCC              768
135 Val Arg Asp Ile Asp  *
136                 245
138 TGGATGTTTG GAAACATTTT TTAAAACAAG CCAAGAAAGA TGTATATAGG TGTGTGAGAC     828
140 TACTAAGAGG CATGGCCCAA CGGTACACGA CTCAGTATCC ATGCTCTTGA CCTTGTAGAG     888
142 AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC ACAATGGTTT     948
144 TTAAATTTTG TAATGAATTC CTAGAATTAA ACCAGATTGG AGCAATTACG GGTTGACCTT    1008
146 ATGAGAAACT GCATGTGGGC TATGGGAGGG GTTGGTCCCT GGTCATGTGC CCCTTCGCAG    1068
148 CTGAAGTGGA GAGGGTGTCA TCTAGCGCAA TTGAAGGATC ATCTGAAGGG GCAAATTCTT    1128
150 TTGAATTGTT ACATCATGCT GGAACCTGCA AAAAATACTT TTTCTAATGA GGAGAGAAAA    1188
152 TATATGTATT TTTATATAAT ATCTAAAGTT ATATTTCAGA TGTAATGTTT TCTTTGCAAA    1248
154 GTATTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA ATATTTAAAA ATGTCTTGCT    1308
156 GTTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCACT TTGTAAATTC    1368
158 CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCCTAATA TCAAATGCAG    1428
160 TATATTTCTT CGTTCTTTTT AAGTTAATAG ATTTTTTCAG ACTTGTCAAG CCTGTGCAAA    1488
162 AAAATTAAAA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT GCCTTTCAAA    1548
164 TTTAGAAACT AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT AATGGGCCAC    1608
166 TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTTCCAC AAGTGCCGCA    1668
168 AATTGTACCT TTTTTTGTTT TTTTCAAAAT AGAAAGTTA TTAGTGGTTT ATCAGCAAAA     1728
170 AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACTGTA CAATAAAAAC ATTGCCTTTG    1788
172 AATGTTAATT TTTTGGTACA AAAGTCGACG GCCGC                               1823
175 (2) INFORMATION FOR SEQ ID NO: 2:
177      (i) SEQUENCE CHARACTERISTICS:
178           (A) LENGTH: 245 amino acids
179           (B) TYPE: amino acid
180           (D) TOPOLOGY: linear
182      (ii) MOLECULE TYPE: protein
184      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
186 Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
187  1               5                   10                  15
189 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
190                 20                  25                  30
192 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
193            35                  40                  45
195 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
196       50                  55                  60
198 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
199  65                  70                  75                  80
201 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
202                 85                  90                  95
204 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
205            100                 105                 110
207 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
208            115                 120                 125
210 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
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RAW SEQUENCE LISTING                    DATE: 02/15/2002
PATENT APPLICATION:  US/10/017,910     TIME: 15:47:44

Input Set : N:\Crf3\RULE60\10017910.txt
Output Set: N:\CRF3\02152002\J017910.raw

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211    130                   135                   140
213 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
214 145                   150                   155                   160
216 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
217                   165                   170                   175
219 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
220                   180                   185                   190
222 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
223                   195                   200                   205
225 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
226       210                   215                   220
228 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
229 225                   230                   235                   240
231 Val Arg Asp Ile Asp
232                   245
234 (2) INFORMATION FOR SEQ ID NO: 3:
236       (i) SEQUENCE CHARACTERISTICS:
237             (A) LENGTH: 2237 base pairs
238             (B) TYPE: nucleic acid
239             (C) STRANDEDNESS: double
240             (D) TOPOLOGY: linear
242       (ii) MOLECULE TYPE: cDNA
244       (iii) HYPOTHETICAL: NO
246       (vi) ORIGINAL SOURCE:
247             (A) ORGANISM: Mus musculus
249       (ix) FEATURE:
250             (A) NAME/KEY: CDS
251             (B) LOCATION: 142..1092
254       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
256 CCCACGTCCC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTCGGGGCG GGGGCCGTGG      60
258 CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG AGCAGGGCGC     120
260 CCGAACTCCG GGCGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG     171
261                         Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys
W--> 262                                         250                   255
264 TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC     219
265 Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His
W--> 266             260                   265                   270
268 GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA     267
269 Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro
W--> 270             275                   280                   285
272 CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG     315
273 Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu
W--> 274             290                   295                   300
276 GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG     363
277 Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln
W--> 278 305                   310                   315                   320
280 ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA     411
281 Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg
W--> 282             325                   330                   335
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        284 ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG      459
        285 Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu
W--> 286            340                 345                 350
        288 AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT      507
        289 Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe
W--> 290            355                 360                 365
        292 CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC      555
        293 Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg
W--> 294            370                 375                 380
        296 TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC      603
        297 Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala
W--> 298 385                390                 395                 400
        300 CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT      651
        301 Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
W--> 302            405                 410                 415
        304 GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG      699
        305 Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp
W--> 306            420                 425                 430
        308 TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC      747
        309 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn
W--> 310            435                 440                 445
        312 GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC      795
        313 Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
W--> 314            450                 455                 460
        316 ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT      843
        317 Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr
W--> 318 465                470                 475                 480
        320 CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT      891
        321 Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser
W--> 322            485                 490                 495
        324 TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT      939
        325 Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn
W--> 326            500                 505                 510
        328 TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC      987
        329 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
W--> 330            515                 520                 525
        332 CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG     1035
        333 Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu
W--> 334            530                 535                 540
        336 GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC     1083
        337 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp
W--> 338 545                550                 555                 560
        340 ATA GAC TGA GACTCATTTC GTGGAACATT AGCATGGATG TCCTAGATGT             1132
        341 Ile Asp  *
        344 TTGGAAACTT CTTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT AAGAGACATG   1192
        346 GCCCACGGTG TATGAAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT TGTGTATATG   1252
        348 TAAAGTCCAT AGGTGATGTT AGATTCATGG TGATTACACA ACGGTTTTAC AATTTTGTAA   1312
        350 TGATTTCCTA GAATTGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA AAAACTTACA   1372
        352 CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT GCCACTGAGA   1432
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VERIFICATION SUMMARY    DATE: 02/15/2002
PATENT APPLICATION: US/10/017,910  TIME: 15:47:45

Input Set : N:\Crf3\RULE60\10017910.txt
Output Set: N:\CRF3\02152002\J017910.raw

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L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:266 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:290 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:298 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:326 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:330 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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